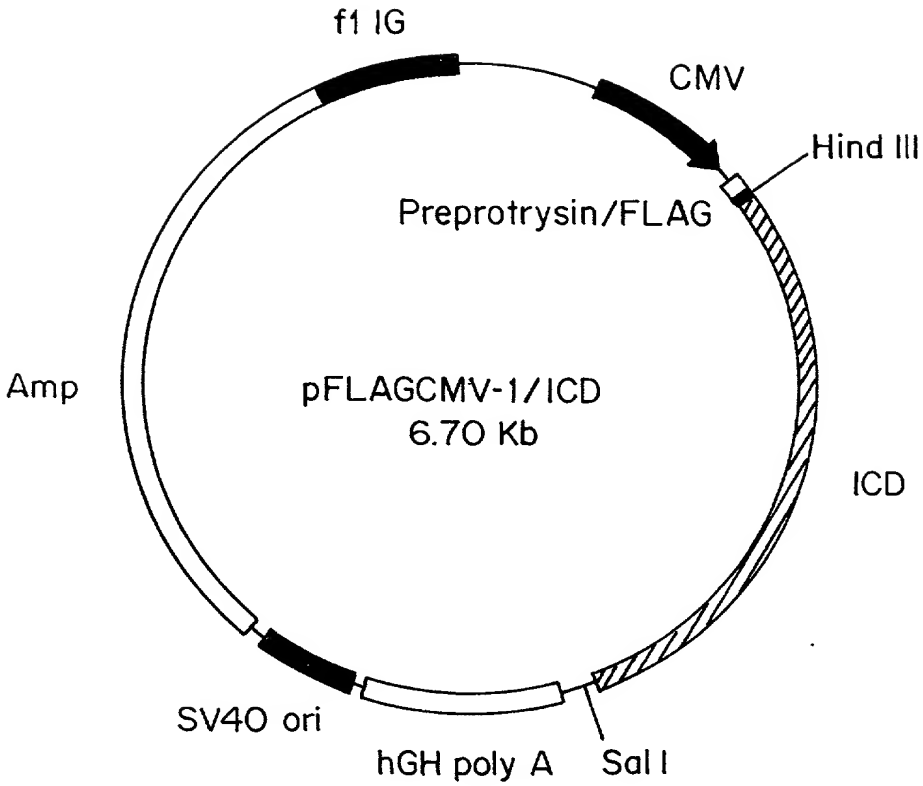

FIG. 1.

09815356 - 020200

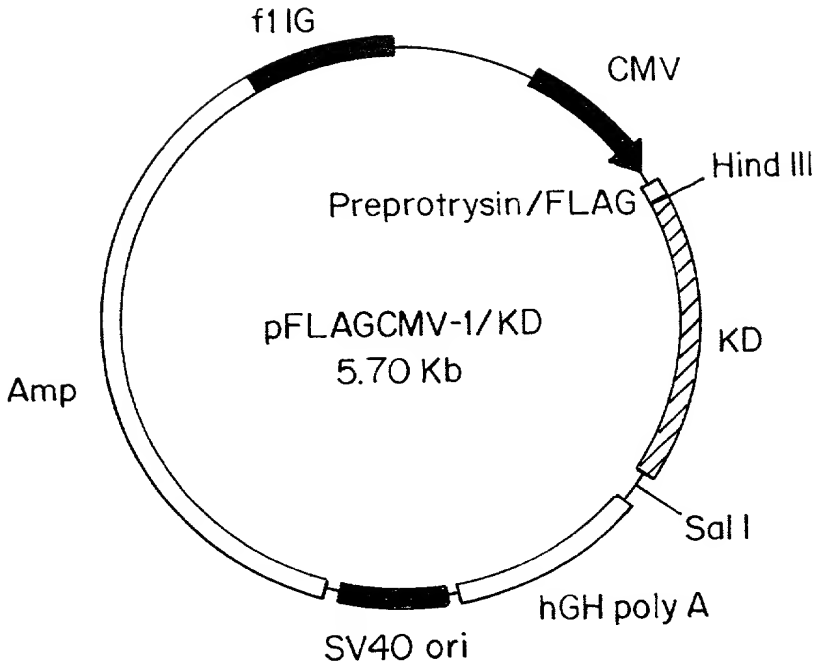
f1 IG
CMV
Hind III
Preprotrysin/FLAG
pFLAGCMV-1/KD
5.70 Kb
KD
Amp
Sal I
hGH poly A
SV40 ori

FIG. 2.

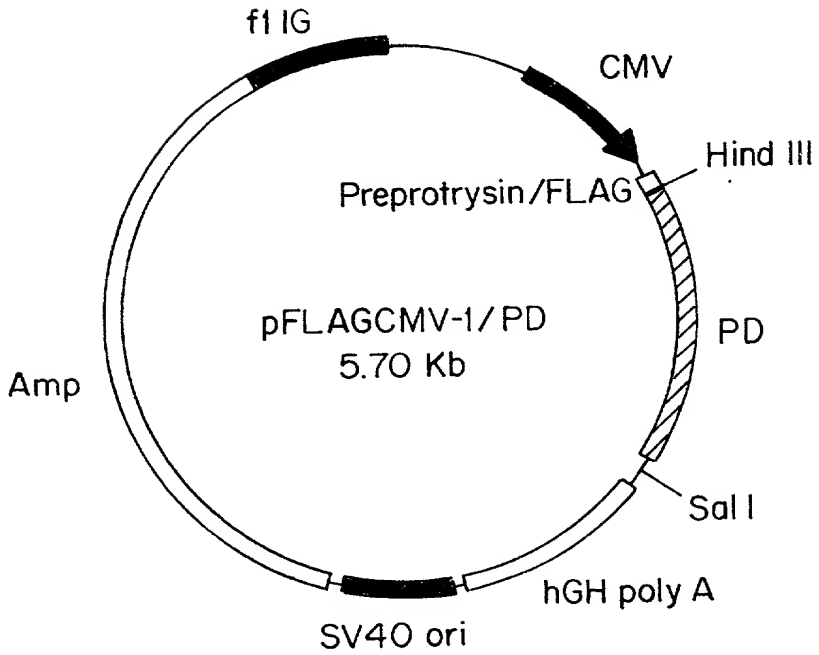
f1 IG
CMV
Hind III
Preprotrysin/FLAG
pFLAGCMV-1/PD
5.70 Kb
PD
Amp
Sal I
hGH poly A
SV40 ori

FIG. 3.

30+020' 95E+5860

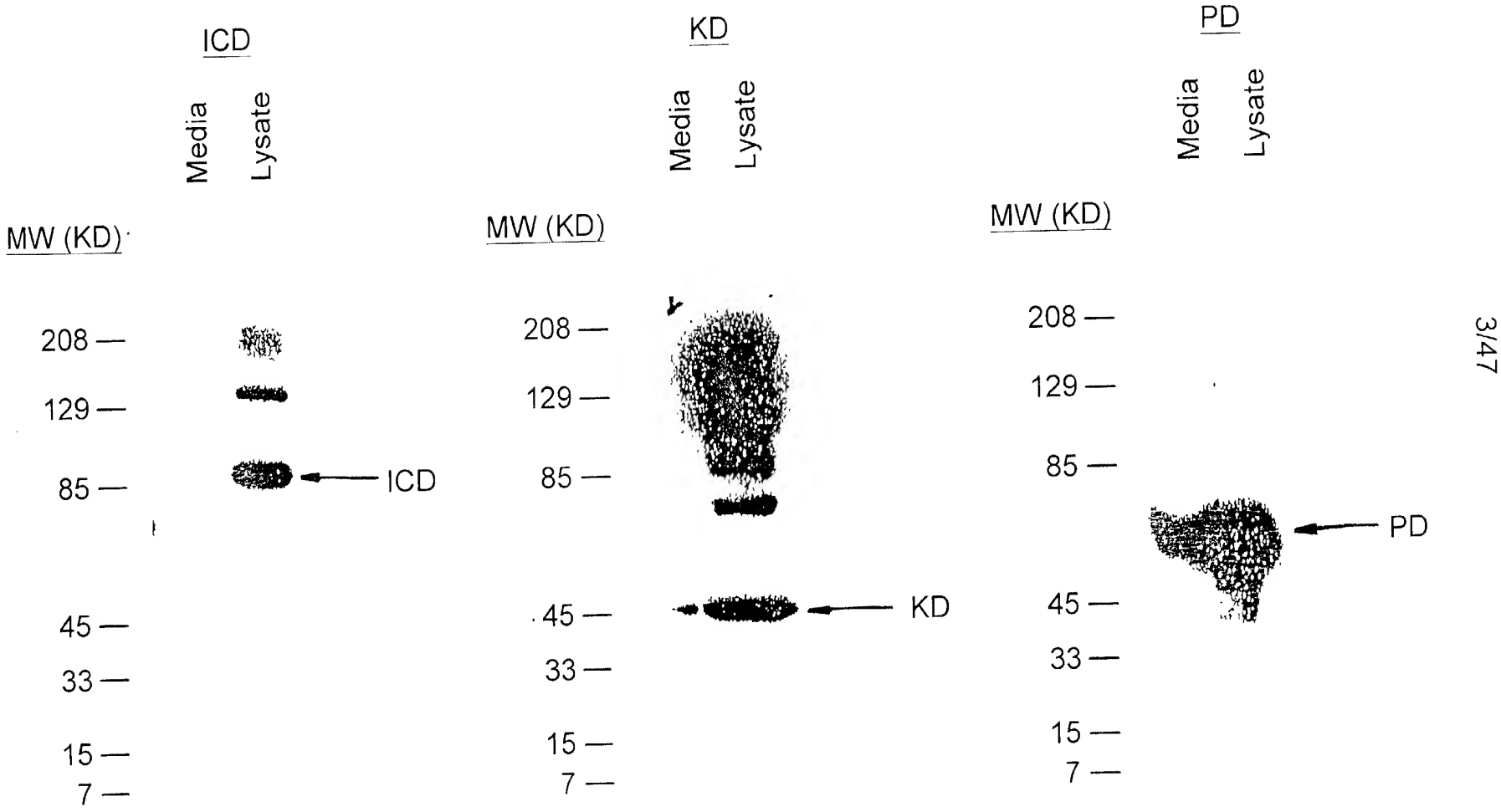

FIG. 4.

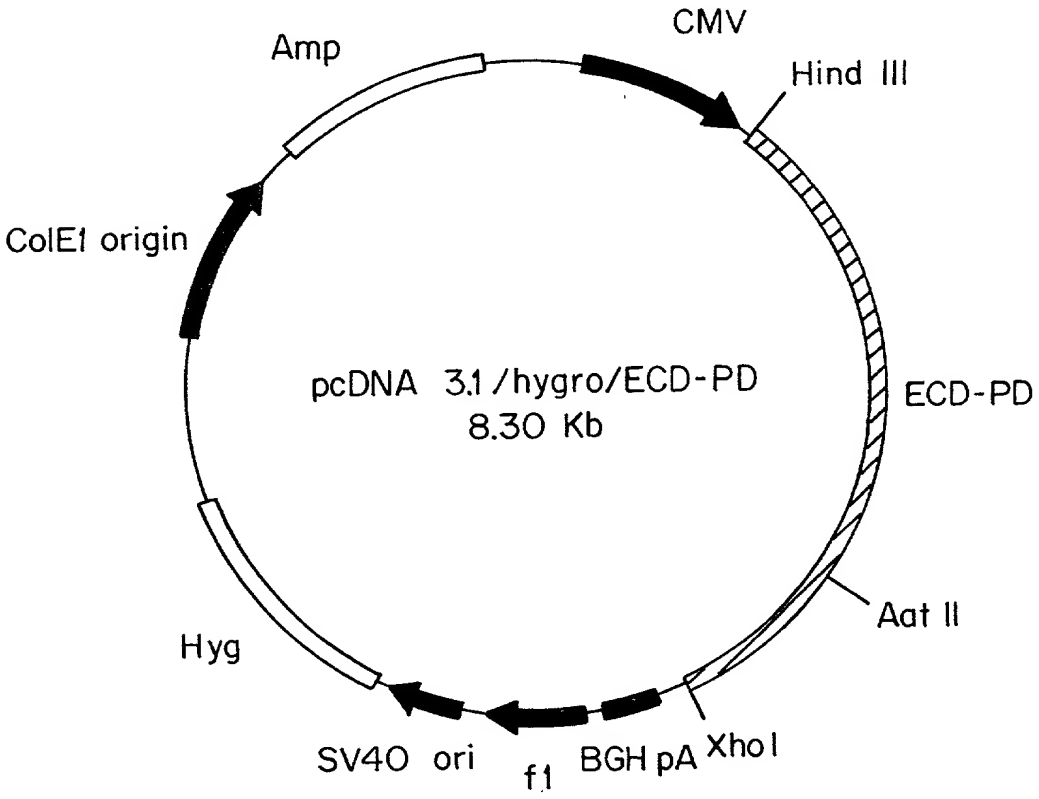
CMV
Amp
Hind III
ColE1 origin
pcDNA 3.1/hygro/ECD-PD
8.30 Kb
ECD-PD
Aat II
Hyg
SV40 ori
f1
BGH pA
Xho I

FIG. 5.

pcDNA3.1hyg/ECD-PD expression

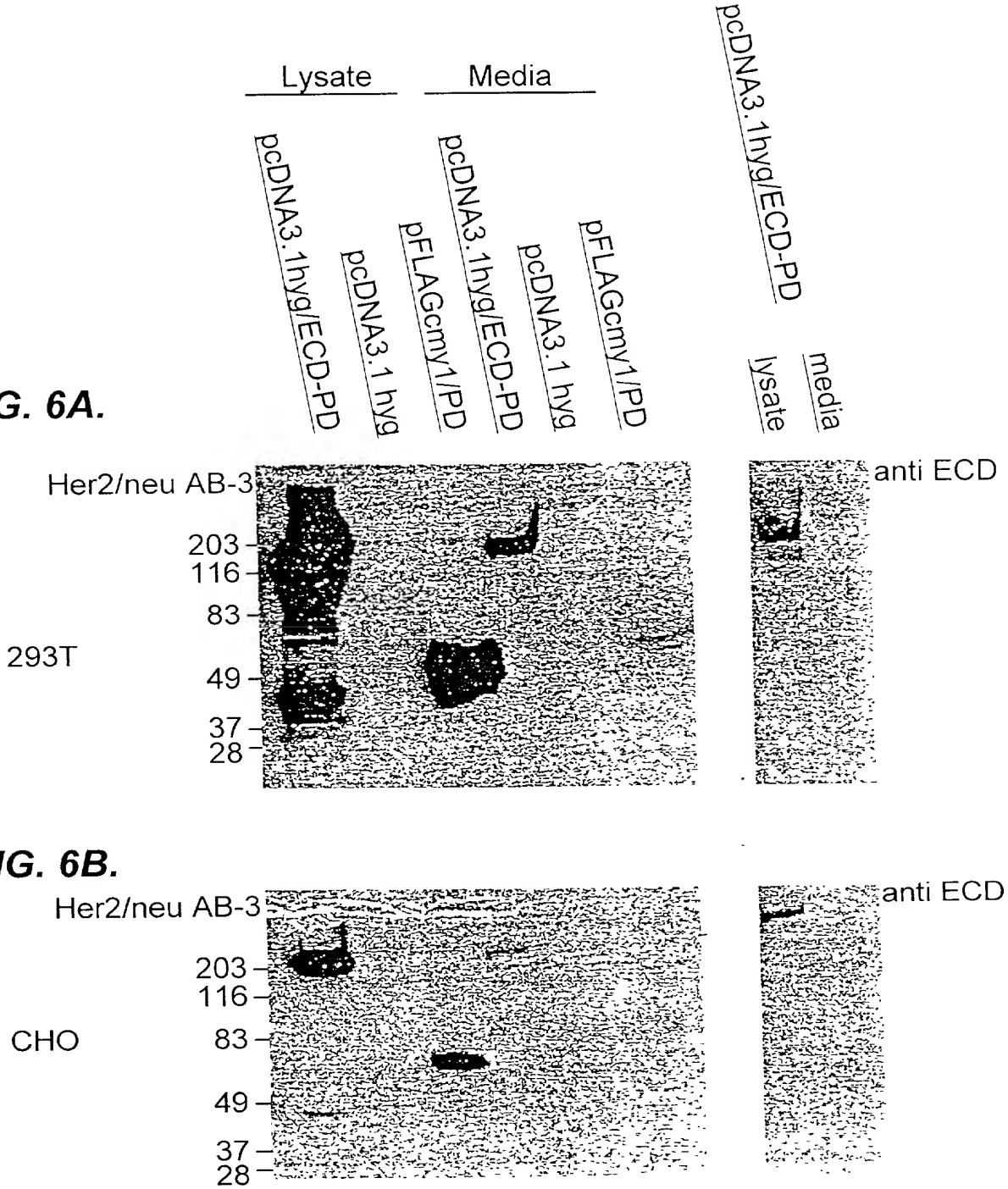

FIG. 6A.

FIG. 6B.

```
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 1               5                  10                  15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
        115                 120                 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    130                 135                 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145                 150                 155                 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
            180                 185                 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255
```

FIG. 7. (SEQ ID NO: 1)

```
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
    290                 295                 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                 470                 475                 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
                485                 490                 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
            500                 505                 510
```

FIG. 7. **(CONTINUED)**

US 2005/0260186 A1

```
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
        515                 520                 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
    530                 535                 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                 550                 555                 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
                565                 570                 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
            580                 585                 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
        595                 600                 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
    610                 615                 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625                 630                 635                 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
                645                 650                 655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
            660                 665                 670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
        675                 680                 685

Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
    690                 695                 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
705                 710                 715                 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
                725                 730                 735

Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
            740                 745                 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
        755                 760                 765
```

FIG. 7. (CONTINUED)

Exhibit 1015, p. 0047

```
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
    770                 775                 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
785                 790                 795                 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
                805                 810                 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
            820                 825                 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
        835                 840                 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
    850                 855                 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865                 870                 875                 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
                885                 890                 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
            900                 905                 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
        915                 920                 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
    930                 935                 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945                 950                 955                 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
                965                 970                 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
            980                 985                 990

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
        995                1000                1005

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
   1010                1015                1020
```

FIG. 7. (CONTINUED)

Substitute Sheet (Rule 26)

```
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
1025                1030                1035                1040

Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
                1045                1050                1055

Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
            1060                1065                1070

Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
        1075                1080                1085

Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
    1090                1095                1100

Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
1105                1110                1115                1120

Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
                1125                1130                1135

Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
            1140                1145                1150

Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
        1155                1160                1165

Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
    1170                1175                1180

Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
1185                1190                1195                1200

Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
                1205                1210                1215

Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
            1220                1225                1230

Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
        1235                1240                1245

Leu Gly Leu Asp Val Pro Val  *    *
    1250                1255     1257
```

FIG. 7. **(CONTINUED)**

US 6,855,800 B2

```
Met Glu Leu Ala Ala Trp Cys Arg Trp Gly Phe Leu Leu Ala Leu Leu
 1               5                  10                  15

Pro Pro Gly Ile Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Val Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Met Leu Ile Ala His Asn Gln Val Lys Arg Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Gln Asp Asn Val Ala Ala
        115                 120                 125

Ser Thr Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg
    130                 135                 140

Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Arg Gly Asn Pro
145                 150                 155                 160

Gln Leu Cys Tyr Gln Asp Met Val Leu Trp Lys Asp Val Phe Arg Lys
                165                 170                 175

Asn Asn Gln Leu Ala Pro Val Asp Ile Asp Thr Asn Arg Ser Arg Ala
            180                 185                 190

Cys Pro Pro Cys Ala Pro Ala Cys Lys Asp Asn His Cys Trp Gly Glu
        195                 200                 205

Ser Pro Glu Asp Cys Gln Ile Leu Thr Gly Thr Ile Cys Thr Ser Gly
    210                 215                 220

Cys Ala Arg Cys Lys Gly Arg Leu Pro Thr Asp Cys Cys His Glu Gln
225                 230                 235                 240

Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys
                245                 250                 255
```

FIG. 8. **(SEQ ID NO:2)**

```
Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu
            260                 265                 270

Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met His Asn Pro Glu Gly
        275                 280                 285

Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Thr Cys Pro Tyr Asn Tyr
    290                 295                 300

Leu Ser Thr Glu Val Gly Ser Cys Thr Leu Val Cys Pro Pro Asn Asn
305                 310                 315                 320

Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser
                325                 330                 335

Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg
            340                 345                 350

Gly Ala Arg Ala Ile Thr Ser Asp Asn Val Gln Glu Phe Asp Gly Cys
        355                 360                 365

Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly
    370                 375                 380

Asp Pro Ser Ser Gly Ile Ala Pro Leu Arg Pro Glu Gln Leu Gln Val
385                 390                 395                 400

Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp
                405                 410                 415

Pro Asp Ser Leu Arg Asp Leu Ser Val Phe Gln Asn Leu Arg Ile Ile
            420                 425                 430

Arg Gly Arg Ile Leu His Asp Gly Ala Tyr Ser Leu Thr Leu Gln Gly
        435                 440                 445

Leu Gly Ile His Ser Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser
    450                 455                 460

Gly Leu Ala Leu Ile His Arg Asn Ala His Leu Cys Phe Val His Thr
465                 470                 475                 480

Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His
                485                 490                 495

Ser Gly Asn Arg Pro Glu Glu Asp Cys Gly Leu Glu Gly Leu Val Cys
            500                 505                 510
```

FIG. 8. **(CONTINUED)**

Docket No. 5155.0020-00

Asn Ser Leu Cys Ala His Gly His Cys Trp Gly Pro Gly Pro Thr Gln
515 520 525

Cys Val Asn Cys Ser His Phe Leu Arg Gly Gln Glu Cys Val Glu Glu
530 535 540

Cys Arg Val Trp Lys Gly Leu Pro Arg Glu Tyr Val Ser Asp Lys Arg
545 550 555 560

Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Ser Ser Glu Thr
565 570 575

Cys Phe Gly Ser Glu Ala Asp Gln Cys Ala Ala Cys Ala His Tyr Lys
580 585 590

Asp Ser Ser Ser Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp
595 600 605

Leu Ser Tyr Met Pro Ile Trp Lys Tyr Pro Asp Glu Glu Gly Ile Cys
610 615 620

Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Glu
625 630 635 640

Arg Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Val Thr Phe Ile Ile
645 650 655

Ala Thr Val Glu Gly Val Leu Leu Phe Leu Ile Leu Val Val Val Val
660 665 670

Gly Ile Leu Ile Lys Arg Arg Arg Gln Lys Ile Arg Lys Tyr Thr Met
675 680 685

Arg Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser
690 695 700

Gly Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu
705 710 715 720

Leu Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr
725 730 735

Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala
740 745 750

Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile
755 760 765

FIG. 8. (CONTINUED)

Exhibit 1015 - Page 13 of 47

Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser
770 775 780

Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln
785 790 795 800

Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu His Arg Gly
805 810 815

Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Val Gln Ile Ala Lys
820 825 830

Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala
835 840 845

Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp
850 855 860

Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala
865 870 875 880

Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu
885 890 895

Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
900 905 910

Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro
915 920 925

Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln
930 935 940

Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp
945 950 955 960

Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu
965 970 975

Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn
980 985 990

Glu Asp Leu Gly Pro Ser Ser Pro Met Asp Ser Thr Phe Tyr Arg Ser
995 1000 1005

Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr
1010 1015 1020

FIG. 8. (CONTINUED)

SUBSTITUTE SHEET (RULE 26)

```
Leu Val Pro Gln Gln Gly Phe Phe Ser Pro Asp Pro Thr Pro Gly Thr
1025                1030                1035                1040

Gly Ser Thr Ala His Arg Arg His Arg Ser Ser Ser Thr Arg Ser Gly
                1045                1050                1055

Gly Gly Glu Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Gly Pro Pro
            1060                1065                1070

Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp
        1075                1080                1085

Gly Asp Leu Ala Met Gly Val Thr Lys Gly Leu Gln Ser Leu Ser Pro
    1090                1095                1100

His Asp Leu Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Leu Pro
1105                1110                1115                1120

Leu Pro Pro Glu Thr Asp Gly Tyr Val Ala Pro Leu Ala Cys Ser Pro
                1125                1130                1135

Gln Pro Glu Tyr Val Asn Gln Ser Glu Val Gln Pro Gln Pro Pro Leu
            1140                1145                1150

Thr Pro Glu Gly Pro Leu Pro Pro Val Arg Pro Ala Gly Ala Thr Leu
        1155                1160                1165

Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
    1170                1175                1180

Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Val Pro
1185                1190                1195                1200

Arg Glu Gly Thr Ala Ser Pro Pro His Pro Ser Pro Ala Phe Ser Pro
                1205                1210                1215

Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asn Ser Ser Glu Gln Gly
            1220                1225                1230

Pro Pro Pro Ser Asn Phe Glu Gly Thr Pro Thr Ala Glu Asn Pro Glu
        1235                1240                1245

Tyr Leu Gly Leu Asp Val Pro Val  *    *
    1250                1255        1258
```

FIG. 8. **(CONTINUED)**

SUBSTITUTE SHEET (RULE 26)

```
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 1               5                  10                  15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
        115                 120                 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    130                 135                 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145                 150                 155                 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
            180                 185                 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255
```

FIG. 9. **(SEQ ID NO: 3)**

```
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
    290                 295                 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                 470                 475                 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
                485                 490                 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
            500                 505                 510
```

FIG. 9. **(CONTINUED)**

SUBSTITUTE SHEET (RULE 26)

```
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
        515                 520                 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
    530                 535                 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                 550                 555                 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
                565                 570                 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
            580                 585                 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
        595                 600                 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
    610                 615                 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625                 630                 635                 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser
                645                 650         653
```

FIG. 9. **(CONTINUED)**

```
Gln Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr
  1               5                  10                  15

Arg Ser Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu
            20                  25                  30

Glu Tyr Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro
        35                  40                  45

Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg
    50                  55                  60

Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu
65                  70                  75                  80

Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val
                85                  90                  95
```

FIG. 10. **(SEQ ID NO: 4)**

```
Phe Asp Gly Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu
            100                 105                 110

Pro Thr His Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr
        115                 120                 125

Val Pro Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys
    130                 135                 140

Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro
145                 150                 155                 160

Pro Ser Pro Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala
                165                 170                 175

Thr Leu Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val
            180                 185                 190

Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu
        195                 200                 205

Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe
    210                 215                 220

Ser Pro Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu
225                 230                 235                 240

Arg Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn
                245                 250                 255

Pro Glu Tyr Leu Gly Leu Asp Val Pro Val  *
            260                 265     267
```

FIG. 10. (CONTINUED)

```
Gln Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr
  1               5                  10                  15

Arg Ser Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu
            20                  25                  30

Glu Tyr Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro
        35                  40                  45

Gly Ala Gly Gly Met Val His His Arg His Arg  *
    50                  55                  60
```

FIG. 11. (SEQ ID NO: 5)

SUBSTITUTE SHEET (RULE 26)

```
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 1               5                  10                  15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
        115                 120                 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    130                 135                 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145                 150                 155                 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
            180                 185                 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255
```

FIG. 12. (SEQ ID NO: 6)

SUBSTITUTE SHEET (RULE 26)

```
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
    290                 295                 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                 470                 475                 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
                485                 490                 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
            500                 505                 510
```

FIG. 12. (CONTINUED)

SUBSTITUTE SHEET (RULE 26)

```
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
        515                 520                 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
    530                 535                 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                 550                 555                 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
                565                 570                 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
            580                 585                 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
        595                 600                 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
    610                 615                 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625                 630                 635                 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Gln Asn Glu
                645                 650                 655

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
            660                 665                 670

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
        675                 680                 685

Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
    690                 695                 700

Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
705                 710                 715                 720

Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
                725                 730                 735

Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
            740                 745                 750

Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
        755                 760                 765
```

FIG. 12. (CONTINUED)

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```
Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
    770                 775                 780

Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
785                 790                 795                 800

Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
                805                 810                 815

Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
            820                 825                 830

Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
        835                 840                 845

Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
    850                 855                 860

Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
865                 870                 875                 880

Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
                885                 890                 895

Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
            900                 905                 910

Leu Gly Leu Asp Val Pro Val  *
        915                 920
```

FIG. 12. **(CONTINUED)**

SUBSTITUTE SHEET (RULE 26)

```
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
 1               5                  10                  15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
        115                 120                 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
    130                 135                 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln
145                 150                 155                 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
            180                 185                 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255
```

FIG. 13. (SEQ ID NO: 7)

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```
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
    290                 295                 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350

Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                 470                 475                 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
                485                 490                 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
            500                 505                 510
```

FIG. 13. **(CONTINUED)**

Substitute Sheet (Rule 26)

```
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
        515                 520                 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
    530                 535                 540

Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                 550                 555                 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
                565                 570                 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
            580                 585                 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
        595                 600                 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
    610                 615                 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625                 630                 635                 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Gln Asn Glu
                645                 650                 655

Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu
            660                 665                 670

Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu
        675                 680                 685

Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly
    690                 695                 700

Gly Met Val His His Arg His Arg  *   *
705                 710             714
```

***FIG. 13.*(CONTINUED)**

```
Met Glu Leu Ala Ala Trp Cys Arg Trp Gly Phe Leu Leu Ala Leu Leu
 1               5                  10                  15

Pro Pro Gly Ile Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Val Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Met Leu Ile Ala His Asn Gln Val Lys Arg Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Gln Asp Asn Val Ala Ala
        115                 120                 125

Ser Thr Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg
    130                 135                 140

Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Arg Gly Asn Pro
145                 150                 155                 160

Gln Leu Cys Tyr Gln Asp Met Val Leu Trp Lys Asp Val Phe Arg Lys
                165                 170                 175

Asn Asn Gln Leu Ala Pro Val Asp Ile Asp Thr Asn Arg Ser Arg Ala
            180                 185                 190

Cys Pro Pro Cys Ala Pro Ala Cys Lys Asp Asn His Cys Trp Gly Glu
        195                 200                 205

Ser Pro Glu Asp Cys Gln Ile Leu Thr Gly Thr Ile Cys Thr Ser Gly
    210                 215                 220

Cys Ala Arg Cys Lys Gly Arg Leu Pro Thr Asp Cys Cys His Glu Gln
225                 230                 235                 240

Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys
                245                 250                 255
```

FIG. 14. (SEQ ID NO: 8)

Substitute Sheet (Rule 26)

```
Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu
            260                 265                 270

Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met His Asn Pro Glu Gly
        275                 280                 285

Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Thr Cys Pro Tyr Asn Tyr
    290                 295                 300

Leu Ser Thr Glu Val Gly Ser Cys Thr Leu Val Cys Pro Pro Asn Asn
305                 310                 315                 320

Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser
                325                 330                 335

Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg
            340                 345                 350

Gly Ala Arg Ala Ile Thr Ser Asp Asn Val Gln Glu Phe Asp Gly Cys
        355                 360                 365

Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly
    370                 375                 380

Asp Pro Ser Ser Gly Ile Ala Pro Leu Arg Pro Glu Gln Leu Gln Val
385                 390                 395                 400

Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp
                405                 410                 415

Pro Asp Ser Leu Arg Asp Leu Ser Val Phe Gln Asn Leu Arg Ile Ile
            420                 425                 430

Arg Gly Arg Ile Leu His Asp Gly Ala Tyr Ser Leu Thr Leu Gln Gly
        435                 440                 445

Leu Gly Ile His Ser Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser
    450                 455                 460

Gly Leu Ala Leu Ile His Arg Asn Ala His Leu Cys Phe Val His Thr
465                 470                 475                 480

Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His
                485                 490                 495

Ser Gly Asn Arg Pro Glu Glu Asp Cys Gly Leu Glu Gly Leu Val Cys
            500                 505                 510
```

FIG. 14. (CONTINUED)

DEMANDE - DEMAND

```
Asn Ser Leu Cys Ala His Gly His Cys Trp Gly Pro Gly Pro Thr Gln
        515                 520                 525

Cys Val Asn Cys Ser His Phe Leu Arg Gly Gln Glu Cys Val Glu Glu
    530                 535                 540

Cys Arg Val Trp Lys Gly Leu Pro Arg Glu Tyr Val Ser Asp Lys Arg
545                 550                 555                 560

Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Ser Ser Glu Thr
                565                 570                 575

Cys Phe Gly Ser Glu Ala Asp Gln Cys Ala Ala Cys Ala His Tyr Lys
            580                 585                 590

Asp Ser Ser Ser Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp
        595                 600                 605

Leu Ser Tyr Met Pro Ile Trp Lys Tyr Pro Asp Glu Glu Gly Ile Cys
    610                 615                 620

Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Glu
625                 630                 635                 640

Arg Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Val Thr Phe
                645                 650                 654
```

FIG. 14. **(CONTINUED)**

Substitute Sheet (Rule 26)

```
ATG GAG CTG GCG GCC TTG TGC CGC TGG GGG CTC CTC CTC GCC CTC    45
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu
 1               5                  10                  15

TTG CCC CCC GGA GCC GCG AGC ACC CAA GTG TGC ACC GGC ACA GAC    90
Leu Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp
            20                  25                  30

ATG AAG CTG CGG CTC CCT GCC AGT CCC GAG ACC CAC CTG GAC ATG   135
Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
        35                  40                  45

CTC CGC CAC CTC TAC CAG GGC TGC CAG GTG GTG CAG GGA AAC CTG   180
Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu
    50                  55                  60

GAA CTC ACC TAC CTG CCC ACC AAT GCC AGC CTG TCC TTC CTG CAG   225
Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln
65                  70                  75

GAT ATC CAG GAG GTG CAG GGC TAC GTG CTC ATC GCT CAC AAC CAA   270
Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln
            80                  85                  90

GTG AGG CAG GTC CCA CTG CAG AGG CTG CGG ATT GTG CGA GGC ACC   315
Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr
        95                  100                 105

CAG CTC TTT GAG GAC AAC TAT GCC CTG GCC GTG CTA GAC AAT GGA   360
Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly
    110                 115                 120

GAC CCG CTG AAC AAT ACC ACC CCT GTC ACA GGG GCC TCC CCA GGA   405
Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly
125                 130                 135

GGC CTG CGG GAG CTG CAG CTT CGA AGC CTC ACA GAG ATC TTG AAA   450
Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
            140                 145                 150

GGA GGG GTC TTG ATC CAG CGG AAC CCC CAG CTC TGC TAC CAG GAC   495
Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp
        155                 160                 165

ACG ATT TTG TGG AAG GAC ATC TTC CAC AAG AAC AAC CAG CTG GCT   540
Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala
    170                 175                 180
```

FIG. 15. (SEQ ID NO:9)

SUBSTITUTE SHEET (RULE 26)

```
CTC ACA CTG ATA GAC ACC AAC CGC TCT CGG GCC TGC CAC CCC TGT  585
Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys
                185                 190                 195

TCT CCG ATG TGT AAG GGC TCC CGC TGC TGG GGA GAG AGT TCT GAG  630
Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu
                200                 205                 210

GAT TGT CAG AGC CTG ACG CGC ACT GTC TGT GCC GGT GGC TGT GCC  675
Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala
                215                 220                 225

CGC TGC AAG GGG CCA CTG CCC ACT GAC TGC TGC CAT GAG CAG TGT  720
Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
                230                 235                 240

GCT GCC GGC TGC ACG GGC CCC AAG CAC TCT GAC TGC CTG GCC TGC  765
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys
                245                 250                 255

CTC CAC TTC AAC CAC AGT GGC ATC TGT GAG CTG CAC TGC CCA GCC  810
Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala
                260                 265                 270

CTG GTC ACC TAC AAC ACA GAC ACG TTT GAG TCC ATG CCC AAT CCC  855
Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
                275                 280                 285

GAG GGC CGG TAT ACA TTC GGC GCC AGC TGT GTG ACT GCC TGT CCC  900
Glu Glu Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro
                290                 295                 300

TAC AAC TAC CTT TCT ACG GAC GTG GGA TCC TGC ACC CTC GTC TGC  945
Tyr Asn Tyr Leu Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys
                305                 310                 315

CCC CTG CAC AAC CAA GAG GTG ACA GCA GAG GAT GGA ACA CAG CGG  990
Pro Leu His Asn Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg
                320                 325                 330

TGT GAG AAG TGC AGC AAG CCC TGT GCC CGA GTG TGC TAT GGT CTG 1035
Cys Glu Lys Cys Ser Lys Pro Cys Ala Arg Val Cys Tyr Gly Leu
                335                 340                 345

GGC ATG GAG CAC TTG CGA GAG GTG AGG GCA GTT ACC AGT GCC AAT 1080
Gly Met Glu His Leu Arg Glu Val Arg Ala Val Thr Ser Ala Asn
                350                 355                 360
```

FIG. 15. **(CONTINUED)**

Substitute Sheet (Rule 26)

```
ATC CAG GAG TTT GCT GGC TGC AAG AAG ATC TTT GGG AGC CTG GCA 1125
Ile Gln Glu Phe Ala Gly Cys Lys Lys Ile Phe Gly Ser Leu Ala
                365                 370                 375

TTT CTG CCG GAG AGC TTT GAT GGG GAC CCA GCC TCC AAC ACT GCC 1170
Phe Leu Pro Glu Ser Phe Asp Gly Asp Pro Ala Ser Asn Thr Ala
                380                 385                 390

CCG CTC CAG CCA GAG CAG CTC CAA GTG TTT GAG ACT CTG GAA GAG 1215
Pro Leu Gln Pro Glu Gln Leu Gln Val Phe Glu Thr Leu Glu Glu
                395                 400                 405

ATC ACA GGT TAC CTA TAC ATC TCA GCA TGG CCG GAC AGC CTG CCT 1260
Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro Asp Ser Leu Pro
                410                 415                 420

GAC CTC AGC GTC TTC CAG AAC CTG CAA GTA ATC CGG GGA CGA ATT 1305
Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg Gly Arg Ile
                425                 430                 435

CTG CAC AAT GGC GCC TAC TCG CTG ACC CTG CAA GGG CTG GGC ATC 1350
Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu Gly Ile
                440                 445                 450

AGC TGG CTG GGG CTG CGC TCA CTG AGG GAA CTG GGC AGT GGA CTG 1395
Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly Leu
                455                 460                 465

GCC CTC ATC CAC CAT AAC ACC CAC CTC TGC TTC GTG CAC ACG GTG 1440
Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
                470                 475                 480

CCC TGG GAC CAG CTC TTT CGG AAC CCG CAC CAA GCT CTG CTC CAC 1485
Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His
                485                 490                 495

ACT GCC AAC CGG CCA GAG GAC GAG TGT GTG GGC GAG GGC CTG GCC 1530
Thr Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala
                500                 505                 510

TGC CAC CAG CTG TGC GCC CGA GGG CAC TGC TGG GGT CCA GGG CCC 1575
Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro
                515                 520                 525

ACC CAG TGT GTC AAC TGC AGC CAG TTC CTT CGG GGC CAG GAG TGC 1620
Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys
                530                 535                 540
```

FIG. 15. **(CONTINUED)**

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```
GTG GAG GAA TGC CGA GTA CTG CAG GGG CTC CCC AGG GAG TAT GTG 1665
Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
                545                 550                 555

AAT GCC AGG CAC TGT TTG CCG TGC CAC CCT GAG TGT CAG CCC CAG 1710
Asn Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln
                560                 565                 570

AAT GGC TCA GTG ACC TGT TTT GGA CCG GAG GCT GAC CAG TGT GTG 1755
Asn Gly Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val
                575                 580                 585

GCC TGT GCC CAC TAT AAG GAC CCT CCC TTC TGC GTG GCC CGC TGC 1800
Ala Cys Ala His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys
                590                 595                 600

CCC AGC GGT GTG AAA CCT GAC CTC TCC TAC ATG CCC ATC TGG AAG 1845
Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys
                605                 610                 615

TTT CCA GAT GAG GAG GGC GCA TGC CAG CCT TGC CCC ATC AAC TGC 1890
Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys
                620                 625                 630

ACC CAC TCC TGT GTG GAC CTG GAT GAC AAG GGC TGC CCC GCC GAG 1935
Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys Pro Ala Glu
                635                 640                 645

CAG AGA GCC AGC CCT CTG ACG TCC ATC ATC TCT GCG GTG GTT GGC 1980
Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser Ala Val Val Gly
                650                 655                 660

ATT CTG CTG GTC GTG GTC TTG GGG GTG GTC TTT GGG ATC CTC ATC 2025
Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu Ile
                665                 670                 675

AAG CGA CGG CAG CAG AAG ATC CGG AAG TAC ACG ATG CGG AGA CTG 2070
Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg Arg Leu
                680                 685                 690

CTG CAG GAA ACG GAG CTG GTG GAG CCG CTG ACA CCT AGC GGA GCG 2115
Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Ala
                695                 700                 705

ATG CCC AAC CAG GCG CAG ATG CGG ATC CTG AAA GAG ACG GAG CTG 2160
Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
                710                 715                 720
```

FIG. 15. (CONTINUED)

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```
AGG AAG GTG AAG GTG CTT GGA TCT GGC GCT TTT GGC ACA GTC TAC 2205
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr
                725                 730                 735

AAG GGC ATC TGG ATC CCT GAT GGG GAG AAT GTG AAA ATT CCA GTG 2250
Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val
                740                 745                 750

GCC ATC AAA GTG TTG AGG GAA AAC ACA TCC CCC AAA GCC AAC AAA 2295
Ala Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys
                755                 760                 765

GAA ATC TTA GAC GAA GCA TAC GTG ATG GCT GGT GTG GGC TCC CCA 2340
Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro
                770                 775                 780

TAT GTC TCC CGC CTT CTG GGC ATC TGC CTG ACA TCC ACG GTG CAG 2385
Tyr Val Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln
                785                 790                 795

CTG GTG ACA CAG CTT ATG CCC TAT GGC TGC CTC TTA GAC CAT GTC 2430
Leu Val Thr Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val
                800                 805                 810

CGG GAA AAC CGC GGA CGC CTG GGC TCC CAG GAC CTG CTG AAC TGG 2475
Arg Glu Asn Arg Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp
                815                 820                 825

TGT ATG CAG ATT GCC AAG GGG ATG AGC TAC CTG GAG GAT GTG CGG 2520
Cys Met Gln Ile Ala Lys Gly Met Ser Tyr Leu Glu Asp Val Arg
                830                 835                 840

CTC GTA CAC AGG GAC TTG GCC GCT CGG AAC GTG CTG GTC AAG AGT 2565
Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser
                845                 850                 855

CCC AAC CAT GTC AAA ATT ACA GAC TTC GGG CTG GCT CGG CTG CTG 2610
Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu
                860                 865                 870

GAC ATT GAC GAG ACA GAG TAC CAT GCA GAT GGG GGC AAG GTG CCC 2655
Asp Ile Asp Glu Thr Glu Tyr His Ala Asp Gly Gly Lys Val Pro
                875                 880                 885

ATC AAG TGG ATG GCG CTG GAG TCC ATT CTC CGC CGG CGG TTC ACC 2700
Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg Arg Arg Phe Thr
                890                 895                 900
```

FIG. 15. (CONTINUED)

Sequence Listing

```
CAC CAG AGT GAT GTG TGG AGT TAT GGT GTG ACT GTG TGG GAG CTG 2745
His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu
                905                 910                 915

ATG ACT TTT GGG GCC AAA CCT TAC GAT GGG ATC CCA GCC CGG GAG 2790
Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala Arg Glu
                920                 925                 930

ATC CCT GAC CTG CTG GAA AAG GGG GAG CGG CTG CCC CAG CCC CCC 2835
Ile Pro Asp Leu Leu Glu Lys Lgy Glu Arg Leu Pro Gln Pro Pro
                935                 940                 945

ATC TGC ACC ATT GAT GTC TAC ATG ATC ATG GTC AAA TGT TGG ATG 2880
Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
                950                 955                 960

ATT GAC TCT GAA TGT CGG CCA AGA TTC CGG GAG TTG GTG TCT GAA 2925
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu
                965                 970                 975

TTC TCC CGC ATG GCC AGG GAC CCC CAG CGC TTT GTG GTC ATC CAG 2970
Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln
                980                 985                 990

AAT GAG GAC TTG GGC CCA GCC AGT CCC TTG GAC AGC ACC TTC TAC 3015
Asn Glu Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr
                995                 1000                1005

CGC TCA CTG CTG GAG GAC GAT GAC ATG GGG GAC CTG GTG GAT GCT 3060
Arg Ser Leu Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala
                1010                1015                1020

GAG GAG TAT CTG GTA CCC CAG CAG GGC TTC TTC TGT CCA GAC CCT 3105
Glu Glu Tyr Leu Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro
                1025                1030                1035

GCC CCG GGC GCT GGG GGC ATG GTC CAC CAC AGG CAC CGC AGC TCA 3150
Ala Pro Gly Ala Gly Gly Met Val His His Arg His Arg Ser Ser
                1040                1045                1050

TCT ACC AGG AGT GGC GGT GGG GAC CTG ACA CTA GGG CTG GAG CCC 3195
Ser Thr Arg Ser Gly Gly Gly Asp Leu Thr Leu Gly Leu Glu Pro
                1055                1060                1065

TCT GAA GAG GAG GCC CCC AGG TCT CCA CTG GCA CCC TCC GAA GGG 3240
Ser Glu Glu Glu Ala Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly
                1070                1075                1080
```

FIG. 15. (CONTINUED)

```
GCT GGC TCC GAT GTA TTT GAT GGT GAC CTG GGA ATG GGG GCA GCC 3285
Ala Gly Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala Ala
                1085                1090                1095

AAG GGG CTG CAA AGC CTC CCC ACA CAT GAC CCC AGC CCT CTA CAG 3330
Lys Gly Leu Gln Ser Leu Pro Thr His Asp Pro Ser Pro Leu Gln
                1100                1105                1110

CGG TAC AGT GAG GAC CCC ACA GTA CCC CTG CCC TCT GAG ACT GAT 3375
Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu Pro Ser Glu Thr Asp
                1115                1120                1125

GGC TAC GTT GCC CCC CTG ACC TGC AGC CCC CAG CCT GAA TAT GTG 3420
Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln Pro Glu Tyr Val
                1130                1135                1140

AAC CAG CCA GAT GTT CGG CCC CAG CCC CCT TCG CCC CGA GAG GGC 3465
Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro Arg Glu Gly
                1145                1150                1155

CCT CTG CCT GCT GCC CGA CCT GCT GGT GCC ACT CTG GAA AGG CCC 3510
Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro
                1160                1165                1170

AAG ACT CTC TCC CCA GGG AAG AAT GGG GTC GTC AAA GAC GTT TTT 3555
Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val Phe
                1175                1180                1185

GCC TTT GGG GGT GCC GTG GAG AAC CCC GAG TAC TTG ACA CCC CAG 3600
Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
                1190                1195                1200

GGA GGA GCT GCC CCT CAG CCC CAC CCT CCT CCT GCC TTC AGC CCA 3645
Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro
                1205                1210                1215

GCC TTC GAC AAC CTC TAT TAC TGG GAC CAG GAC CCA CCA GAG CGG 3690
Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg
                1220                1225                1230

GGG GCT CCA CCC AGC ACC TTC AAA GGG ACA CCT ACG GCA GAG AAC 3735
Gly Ala Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn
                1235                1240                1245

CCA GAG TAC CTG GGT CTG GAC GTG CCA GTG TGA                  3768
Pro Glu Tyr Leu Gly Leu Asp Val Pro Val
                1250                1255
```

FIG. 15. **(CONTINUED)**

Doc Code: Appeal Brief

```
ccgggccgga gccgcaatga tcatcatgga gctggcggcc tggtgccgct 50
gggggttcct cctcgccctc ctgccccccg gaatcgcggg cacccaagtg 100
tgtaccggca cagacatgaa gttgcggctc cctgccagtc ctgagaccca 150
cctggacatg ctccgccacc tgtaccaggg ctgtcaggta gtgcagggca 200
acttggagct tacctacgtg cctgccaatg ccagcctctc attcctgcag 250
gacatccagg aagttcaggg ttacatgctc atcgctcaca accaggtgaa 300
gcgcgtccca ctgcaaaggc tgcgcatcgt gagagggacc cagctctttg 350
aggacaagta tgccctggct gtgctagaca accgagatcc tcaggacaat 400
gtcgccgcct ccaccccagg cagaacccca gaggggctgc gggagctgca 450
gcttcgaagt ctcacagaga tcctgaaggg aggagttttg atccgtggga 500
accctcagct ctgctaccag gacatggttt tgtggaagga cgtcttccgc 550
aagaataacc aactggctcc tgtcgatata gacaccaatc gttcccgggc 600
ctgtccacct tgtgccccca cctgcaaaga caatcactgt tggggtgaga 650
gtccggaaga ctgtcagatc ttgactggca ccatctgtac cagtggttgt 700
gcccggtgca agggccggct gcccactgac tgctgccatg agcagtgtgc 750
cgcaggctgc acgggcccca agcattctga ctgcctggcc tgcctccact 800
tcaatcatag tggtatctgt gagctgcact gcccagccct cgtcacctac 850
aacacagaca cctttgagtc catgcacaac cctgagggtc gctacacctt 900
tggtgccagc tgcgtgacca cctgccccta caactacctg tctacggaag 950
tgggatcctg cactctggtg tgtcccccga ataaccaaga ggtcacagct 1000
gaggacggaa cacagcgttg tgagaaatgc agcaagccct gtgctcgagt 1050
gtgctatggt ctgggcatgg agcaccttcg aggggcgagg gccatcacca 1100
gtgacaatgt ccaggagttt gatggctgca agaagatctt tgggagcctg 1150
gcatttttgc cggagagctt tgatggggac ccctcctccg gcattgctcc 1200
gctgaggcct gagcagctcc aagtgttcga aaccctggag gagatcacag 1250
gttacctgta catctcagca tggccagaca gtctccgtga cctcagtgtc 1300
ttccagaacc ttcgaatcat tcggggacgg attctccacg atggcgcgta 1350
ctcattgaca ctgcaaggcc tggggatcca ctcgctgggg ctgcgctcac 1400
tgcgggagct gggcagtgga ttggctctga ttcaccgcaa cgcccatctc 1450
tgctttgtac acactgtacc ttgggaccag ctcttccgga acccacatca 1500
ggccctgctc cacagtggga accggccgga agaggacttg tgcgtctcga 1550
gcggcttggt ctgtaactca ctgtgtgccc acgggcactg ctgggggcca 1600
gggcccaccc agtgtgtcaa ctgcagtcat ttccttcggg gccaggagtg 1650
tgtggaggag tgccgagtat ggaaggggct cccccgggag tatgtgagtg 1700
acaagcgctg tctgccgtgt caccccgagt gtcagcctca aaacagctca 1750
gagacctgct ttggatcgga ggctgatcag tgtgcagcct gcgcccacta 1800
caaggactcg tcctcctgtg tggctcgctg ccccagtggt gtgaaaccgg 1850
acctctccta catgcccatc tggaagtacc cggatgagga gggcatatgc 1900
cagccgtgcc ccatcaactg cacccactcc tgtgtggatc tggatgaacg 1950
aggctgccca gcagagcaga gagccagccc ggtgacattc atcattgcaa 2000
ctgtagaggg cgtcctgctg ttcctgatct tagtggtggt cgttggaatc 2050
ctaatcaaac gaaggagaca gaagatccgg aagtatacga tgcgtaggct 2100
gctgcaggaa actgagttag tggagccgct gacgcccagc ggagcaatgc 2150
ccaaccaggc tcagatgcgg atcctaaaag agacggagct aaggaaggtg 2200
aaggtgcttg gatcaggagc ttttggcact gtctacaagg gcatctggat 2250
cccagatggg gagaatgtga aaatccccgt ggctatcaag gtgttgagag 2300
aaaacacatc tcctaaagcc aacaaagaaa ttctagatga agcgtatgtg 2350
```

FIG. 16. **(SEQ ID NO: 10)**

Replacement Sheet

```
atggctggtg tgggttctcc gtatgtgtcc cgcctcctgg gcatctgcct 2400
gacatccaca gtacagctgg tgacacagct tatgccctac ggctgccttc 2450
tggaccatgt ccgagaacac cgaggtcgcc taggctccca ggacctgctc 2500
aactggtgtg ttcagattgc caaggggatg agctacctgg aggacgtgcg 2550
gcttgtacac agggacctgg ctgcccggaa tgtgctagtc aagagtccca 2600
accacgtcaa gattacagat ttcgggctgg ctcggctgct ggacattgat 2650
gagacagagt accatgcaga tgggggcaag gtgcccatca aatggatggc 2700
attggaatct attctcagac gccggttcac ccatcagagt gatgtgtgga 2750
gctatggagt gactgtgtgg gagctgatga cttttggggc caaaccttac 2800
gatggaatcc cagcccggga gatccctgat ttgctggaga agggagaacg 2850
cctacctcag cctccaatct gcaccattga tgtctacatg attatggtca 2900
aatgttggat gattgactct gaatgtcgcc cgagattccg ggagttggtg 2950
tcagaatttt cacgtatggc gagggacccc cagcgttttg tggtcatcca 3000
gaacgaggac ttgggcccat ccagccccat ggacagtacc ttctaccgtt 3050
cactgctgga agatgatgac atgggtgacc tggtagacgc tgaagagtat 3100
ctggtgcccc agcagggatt cttctccccg gaccctaccc caggcactgg 3150
gagcacagcc catagaaggc accgcagctc gtccaccagg agtggaggtg 3200
gtgagctgac actgggcctg gagccctcgg aagaagggcc ccccagatct 3250
ccactggctc cctcggaagg ggctggctcc gatgtgtttg atggtgacct 3300
ggcaatgggg gtaaccaaag ggctgcagag cctctctcca catgacctca 3350
gccctctaca gcggtacagc gaggacccca cattacctct gccccccgag 3400
actgatggct atgttgctcc cctggcctgc agcccccagc ccgagtatgt 3450
gaaccaatca gaggttcagc ctcagcctcc tttaacccca gagggtcctc 3500
tgcctcctgt ccggcctgct ggtgctactc tagaaagacc caagactctc 3550
tctcctggga agaatggggt tgtcaaagac gtttttgcct tcgggggtgc 3600
tgtggagaac cctgaatact tagtaccgag agaaggcact gcctctccgc 3650
cccacccttc tcctgccttc agcccagcct ttgacaacct ctattactgg 3700
gaccagaact catcggagca ggggcctcca ccaagtaact ttgaagggac 3750
ccccactgca gagaaccctg agtacctagg cctggatgta cctgtatgag 3800
acgtgtgcag acgtcctgtg ctttcagagt ggggaaggcc tgacttgtgg 3850
tctccatcgc cacaaagcag ggagagggtc ctctggccac attacatcca 3900
gggcagacgg ctctaccagg aacctgcccc gaggaacctt tccttgctgc 3850
ttgaa      3955
```

FIG. 16. **(CONTINUED)**

Replacement Sheet - 38/47

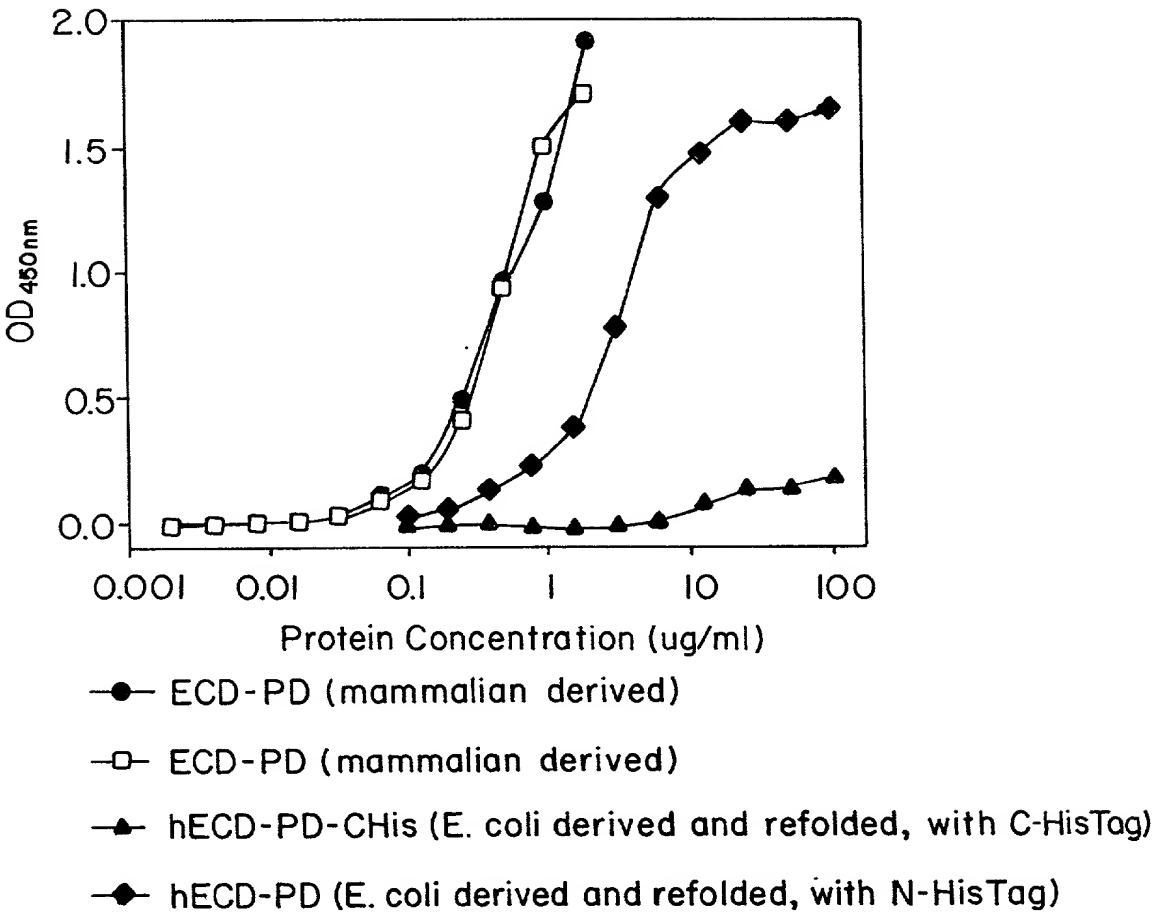
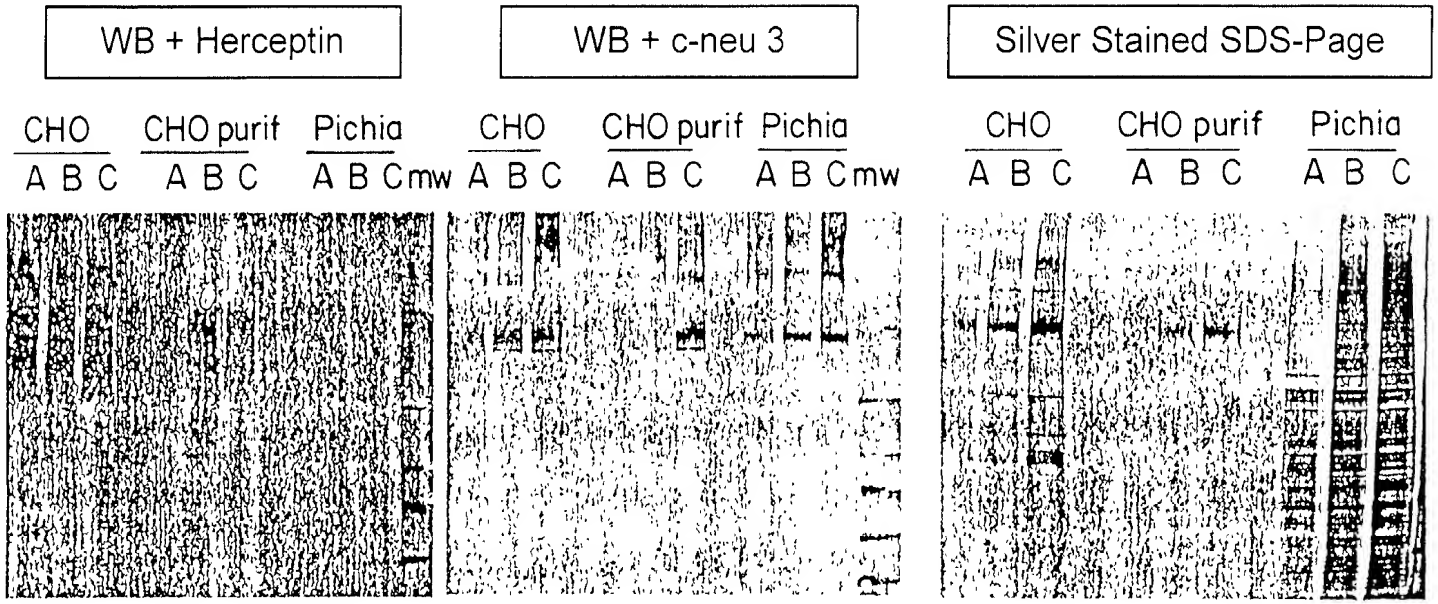

Herceptin Binding by Direct Elisa 10/5/99
2.0
1.5
1.0
0.5
0.0
OD450nm
0.001
0.01
0.1
1
10
100
Protein Concentration (ug/ml)
ECD-PD (mammalian derived)
ECD-PD (mammalian derived)
hECD-PD-CHis (E. coli derived and refolded, with C-HisTag)
hECD-PD (E. coli derived and refolded, with N-HisTag)

FIG. 17.

Comparison of Her2neu ECD-PD Expression in CHO-K1 (S/SF) and Pichia (Non reducing conditions)



Legend: CHO; A, B, C = 2,5µl/ 5µl/ 10µl
CHO purif; A, B, C = 125ng/ 250ng/ 500ng
Pichia; A, B, C = 2,5µl/ 5µl/ 10µl from a 1/30 dilution of OD 120

FIG. 18.

```
atggagctgg cggcctggtg ccgttggggg ttcctcctcg ccctcctgtc 50
ccccggagcc gcgggtaccc aagtgtgtac cggtaccgac atgaagttgc 100
gactccctgc cagtcctgag acccacctgg acatgcttcg ccacctctac 150
cagggctgtc aggtggtgca gggcaatttg gagcttacct acctgcccgc 200
caatgccagc ctctcattcc tgcaggacat ccaggaagtc cagggataca 250
tgctcatcgc tcacaaccga gtgaaacacg tcccactgca gaggttgcgc 300
atcgtgagag ggactcagct ctttgaggac aagtatgccc tggctgtgct 350
agacaaccga gacccttttgg acaacgtcac caccgccgcc ccaggcagaa 400
ccccagaagg gctgcgggag ctgcagcttc gaagtctcac agagatcttg 450
aagggaggag ttttgatccg tgggaaccct cagctctgct accaggacat 500
ggttttgtgg aaggatgtcc tccgtaagaa taaccagctg gctcctgtcg 550
acatggacac caatcgttcc cgggcctgtc caccttgtgc cccaacctgc 600
aaagacaatc actgttgggg tgagagtcct gaagactgtc agatcttgac 650
tggcaccatc tgtactagtg gctgtgcccg gtgcaagggc cggctgccca 700
ctgactgttg ccatgagcag tgtgctgcag gctgcacggg tcccaagcat 750
tctgactgcc tggcctgcct ccacttcaat catagtggta tctgtgagct 800
gcactgcccg gccctcatca cctacaacac agacaccttc gagtccatgc 850
tcaaccctga gggtcgctac acctttggtg ccagctgtgt gaccacctgc 900
ccctacaact acctctccac ggaagtggga tcctgcactc tggtctgtcc 950
cccgaacaac caagaggtca cagctgagga cggaacacag cggtgtgaga 1000
aatgcagcaa gccctgtgct ggagtatgct atggtctggg catggagcac 1050
ctccgagggg cgagggccat caccagtgac aatatccagg agtttgctgg 1100
ctgcaagaag atctttggga gcctggcatt tttgccggag agctttgatg 1150
ggaacccctc ctccggcgtt gccccactga agccagagca tctccaagtg 1200
ttcgaaaccc tggaggagat cacaggttac ctatacattt cagcatggcc 1250
agagagcttc caagacctca gtgtcttcca gaaccttcgg gtcattcggg 1300
gacggattct ccatgatggt gcttactcat tgacgttgca aggcctgggg 1350
attcactcac tggggctacg ctcactgcgg gagctgggca gtggattggc 1400
tctcattcac cgcaacaccc atctctgctt tgtaaacact gtaccttggg 1450
accagctctt ccggaacccg caccaggccc tactccacag tgggaaccgg 1500
ccagaagagg catgtggtct tgagggcttg gtctgtaact cactgtgtgc 1550
ccgtgggcac tgctgggggc cagggcccac ccagtgtgtc aactgcagtc 1600
agttcctccg gggccaggag tgtgtggagg agtgccgagt atggaagggg 1650
ctccccaggg agtatgtgag gggcaagcac tgtctgccat gccaccccga 1700
gtgtcagcct caaaacagct cggagacctg ctatggatcg gaggctgacc 1750
agtgtgaggc ttgtgcccac tacaaggact catcttcctg tgtggctcgc 1800
tgccccagtg gtgtgaagcc agacctctcc tacatgccta tctggaagta 1850
cccggatgag gagggcatat gtcagccatg ccccatcaac tgcacccact 1900
catgtgtgga cctggacgaa cgaggctgcc cagcagagca gagagccagc 1950
ccagtgacat tcatcattgc aactgtggtg ggcgtcctgt tgttcctgat 2000
catagtggtg gtcattggaa tcctaatcaa acgaaggcga cagaagatcc 2050
ggaagtatac catgcgtagg ctgctgcagg agaccgagct ggtggagccg 2100
ctgacgccca gtggagctgt gcccaaccag gctcagatgc ggatcctaaa 2150
ggagacagag ctaaggaagc tgaaggtgct tgggtcagga gccttcggca 2200
ctgtctacaa gggcatctgg atcccagatg gggagaacgt gaaaatcccc 2250
gtggccatca aggtgttgag ggaaaacaca tctcctaaag ctaacaaaga 2300
aatcctagat gaagcgtacg tcatggctgg tgtgggttct ccatatgtgt 2350
```

FIG. 19. **(SEQ ID NO: 11)**

```
cccgcctcct gggcatctgc ctgacatcca cagtgcagct ggtgacacag 2400
cttatgccct atggctgcct tctggaccat gtccgagaac accgaggtcg 2450
cttaggctcc caggacctgc tcaactggtg tgttcagatt gccaagggga 2500
tgagctacct ggaggaagtt cggcttgttc acagggacct agctgcccga 2550
aacgtgctag tcaagagtcc caaccacgtc aagattaccg acttcgggct 2600
ggcacggctg ctggacattg atgagactga ataccatgca gatgggggca 2650
aggtgcccat caagtggatg gcattggaat ctattctcag acgccggttc 2700
actcatcaga gtgatgtgtg gagctatggt gtgactgtgt gggagctgat 2750
gacctttggg gccaaacctt acgatgggat cccagctcgg gagatccctg 2800
atttgctgga gaagggagaa cgcctacctc agcctccaat ctgcaccatc 2850
gacgtctaca tgatcatggt caaatgttgg atgattgact ccgaatgtcg 2900
cccgagattc cgggagttgg tatcagaatt ctcccgtatg gcaagggacc 2950
cccagcgctt tgtggtcatc cagaacgagg acttaggccc ctccagcccc 3000
atggacagca ccttctaccg ttcactgctg gaggatgatg acatgggggga 3050
gctggtcgat gctgaagagt acctggtacc ccagcaggga ttcttctccc 3100
cagaccctgc cctaggtact gggagcacag cccaccgcag acaccgcagc 3150
tcgtcggcca ggagtggcgg tggtgagctg acactgggcc tggagccctc 3200
ggaagaagag ccccccagat ctccactggc tccctccgaa ggggctggct 3250
ccgatgtgtt tgatggtgac ctggcagtgg gggtaaccaa aggactgcag 3300
agcctctctc cacatgacct cagccctcta cagcggtaca gtgaggatcc 3350
cacattacct ctgccccccg agactgatgg ctacgttgct cccctggcct 3400
gcagccccca gcccgagtat gtgaaccagc cagaggttcg gcctcagtct 3450
cccttgaccc cagagggtcc tccgcctccc atccgacctg ctggtgctac 3500
tctagaaaga cccaagactc tctctcctgg gaaaaatggg gttgtcaaag 3550
acgtttttgc ctttgggggt gctgtggaga accctgaata cctagcaccc 3600
agagcaggca ctgcctctca gccccaccct tctcctgcct tcagcccagc 3650
ctttgacaac ctctattact gggaccagaa ctcatcggag cagggtcctc 3700
caccaagtac ctttgaaggg acccccactg cagagaaccc tgagtaccta 3750
ggcctggatg tgccagtatg a                                 3771
```

***FIG. 19.*(CONTINUED)**

Application - Copy

```
Met Glu Leu Ala Ala Trp Cys Arg Trp Gly Phe Leu Leu Ala Leu Leu
 1               5                  10                  15

Ser Pro Gly Ala Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys
            20                  25                  30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
        35                  40                  45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
    50                  55                  60

Leu Pro Ala Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65                  70                  75                  80

Gln Gly Tyr Met Leu Ile Ala His Asn Arg Val Lys His Val Pro Leu
                85                  90                  95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Lys Tyr
            100                 105                 110

Ala Leu Ala Val Leu Asp Asn Arg Asp Pro Leu Asp Asn Val Thr Thr
        115                 120                 125

Ala Ala Pro Gly Arg Thr Pro Glu Gly Leu Arg Glu Leu Gln Leu Arg
    130                 135                 140

Ser Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Arg Gly Asn Pro
145                 150                 155                 160

Gln Leu Cys Tyr Gln Asp Met Val Leu Trp Lys Asp Val Leu Arg Lys
                165                 170                 175

Asn Asn Gln Leu Ala Pro Val Asp Met Asp Thr Asn Arg Ser Arg Ala
            180                 185                 190

Cys Pro Pro Cys Ala Pro Thr Cys Lys Asp Asn His Cys Trp Gly Glu
        195                 200                 205

Ser Pro Glu Asp Cys Gln Ile Leu Thr Gly Thr Ile Cys Thr Ser Gly
    210                 215                 220

Cys Ala Arg Cys Lys Gly Arg Leu Pro Thr Asp Cys Cys His Glu Gln
225                 230                 235                 240

Cys Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys
                245                 250                 255
```

FIG. 20. **(SEQ ID NO: 14)**

```
Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu
            260                 265                 270

Ile Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Leu Asn Pro Glu Gly
        275                 280                 285

Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Thr Cys Pro Tyr Asn Tyr
    290                 295                 300

Leu Ser Thr Glu Val Gly Ser Cys Thr Leu Val Cys Pro Pro Asn Asn
305                 310                 315                 320

Gln Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser
                325                 330                 335

Lys Pro Cys Ala Gly Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg
            340                 345                 350

Gly Ala Arg Ala Ile Thr Ser Asp Asn Ile Gln Glu Phe Ala Gly Cys
        355                 360                 365

Lys Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly
    370                 375                 380

Asn Pro Ser Ser Gly Val Ala Pro Leu Lys Pro Glu His Leu Gln Val
385                 390                 395                 400

Phe Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp
                405                 410                 415

Pro Glu Ser Phe Gln Asp Leu Ser Val Phe Gln Asn Leu Arg Val Ile
            420                 425                 430

Arg Gly Arg Ile Leu His Asp Gly Ala Tyr Ser Leu Thr Leu Gln Gly
        435                 440                 445

Leu Gly Ile His Ser Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser
    450                 455                 460

Gly Leu Ala Leu Ile His Arg Asn Thr His Leu Cys Phe Val Asn Thr
465                 470                 475                 480

Val Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His
                485                 490                 495

Ser Gly Asn Arg Pro Glu Glu Ala Cys Gly Leu Glu Gly Leu Val Cys
            500                 505                 510
```

FIG. 20. (CONTINUED)

```
Asn Ser Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln
        515                 520                 525

Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu
    530                 535                 540

Cys Arg Val Trp Lys Gly Leu Pro Arg Glu Tyr Val Arg Gly Lys His
545                 550                 555                 560

Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Ser Ser Glu Thr
                565                 570                 575

Cys Tyr Gly Ser Glu Ala Asp Gln Cys Glu Ala Cys Ala His Tyr Lys
            580                 585                 590

Asp Ser Ser Ser Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp
        595                 600                 605

Leu Ser Tyr Met Pro Ile Trp Lys Tyr Pro Asp Glu Glu Gly Ile Cys
    610                 615                 620

Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Glu
625                 630                 635                 640

Arg Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Val Thr Phe Ile Ile
                645                 650                 655

Ala Thr Val Val Gly Val Leu Leu Phe Leu Ile Ile Val Val Val Ile
            660                 665                 670

Gly Ile Leu Ile Lys Arg Arg Arg Gln Lys Ile Arg Lys Tyr Thr Met
        675                 680                 685

Arg Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser
    690                 695                 700

Gly Ala Val Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu
705                 710                 715                 720

Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr
                725                 730                 735

Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala
            740                 745                 750

Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile
        755                 760                 765
```

FIG. 20. (CONTINUED)

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```
Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser
    770                 775                 780

Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln
785                 790                 795                 800

Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu His Arg Gly
                805                 810                 815

Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Val Gln Ile Ala Lys
            820                 825                 830

Gly Met Ser Tyr Leu Glu Glu Val Arg Leu Val His Arg Asp Leu Ala
        835                 840                 845

Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp
    850                 855                 860

Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala
865                 870                 875                 880

Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu
                885                 890                 895

Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
            900                 905                 910

Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro
        915                 920                 925

Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln
    930                 935                 940

Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp
945                 950                 955                 960

Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu
                965                 970                 975

Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn
            980                 985                 990

Glu Asp Leu Gly Pro Ser Ser Pro Met Asp Ser Thr Phe Tyr Arg Ser
        995                1000                1005

Leu Leu Glu Asp Asp Asp Met Gly Glu Leu Val Asp Ala Glu Glu Tyr
   1010                1015                1020
```

FIG. 20. (CONTINUED)

```
Leu Val Pro Gln Gln Gly Phe Phe Ser Pro Asp Pro Ala Leu Gly Thr
1025                1030                1035                1040

Gly Ser Thr Ala His Arg Arg His Arg Ser Ser Ser Ala Arg Ser Gly
                1045                1050                1055

Gly Gly Glu Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Pro Pro
            1060                1065                1070

Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp
        1075                1080                1085

Gly Asp Leu Ala Val Gly Val Thr Lys Gly Leu Gln Ser Leu Ser Pro
    1090                1095                1100

His Asp Leu Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Leu Pro
1105                1110                1115                1120

Leu Pro Pro Glu Thr Asp Gly Tyr Val Ala Pro Leu Ala Cys Ser Pro
                1125                1130                1135

Gln Pro Glu Tyr Val Asn Gln Pro Glu Val Arg Pro Gln Ser Pro Leu
            1140                1145                1150

Thr Pro Glu Gly Pro Pro Pro Pro Ile Arg Pro Ala Gly Ala Thr Leu
        1155                1160                1165

Glu Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
    1170                1175                1180

Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Ala Pro
1185                1190                1195                1200

Arg Ala Gly Thr Ala Ser Gln Pro His Pro Ser Pro Ala Phe Ser Pro
                1205                1210                1215

Ala Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asn Ser Ser Glu Gln Gly
            1220                1225                1230

Pro Pro Pro Ser Thr Phe Glu Gly Thr Pro Thr Ala Glu Asn Pro Glu
        1235                1240                1245

Tyr Leu Gly Leu Asp Val Pro Val
    1250                1255
```

FIG. 20. **(CONTINUED)**

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